

From: "Brooke Watson" <watson@ecohealthalliance.org>
Sent: 06/29/2017 10:23:05 AM (-07:00)
To: "Tracey Goldstein" <tgoldstein@ucdavis.edu>
Cc: [REDACTED] "Peter Daszak" <daszak@ecohealthalliance.org>; "Jonna Mazet" <jkmazet@ucdavis.edu>; "David John Wolking" <djwolking@ucdavis.edu>; "Christine Kreuder Johnson" <ckjohnson@ucdavis.edu>
Subject: Re: GVP country budget call 3pm PDT/6pm EST

Hi Tracey,

Good point. It's my understanding that these numbers are based on 9 viral families (supplementary materials from mBio [here](#)):

"Laboratory costs included: sample extraction; cDNA synthesis; PCR testing for 7079 samples (nine viral families); cloning and sequencing for ~326 PCR positive samples per 1000 tested (based on number of positive samples in this study); and labor costs for two technicians to perform the work over one year. Total laboratory costs were estimated to be ~US\$850,000.

We calculated field costs based on 3.5 years with 71 sampling trips to collect 7079 samples. At an average cost of \$2,800 per trip (including transport, accommodation, equipment, liquid nitrogen and food), and including labor costs of 4 field staff we estimated total field costs to be ~US\$300,000."

On Thu, Jun 29, 2017 at 12:49 PM, Tracey Goldstein <tgoldstein@ucdavis.edu> wrote:
Hi Brooke,

Thank you for the update. Remember, those estimates that Simon made in his paper were per *viral family* for a few different viral families, and there were differences for each viral family. Did you take that into account? It sounds to me that the numbers you may be using are for one viral family, so just wanted to check?

Best, Tracey

On Thu, Jun 29, 2017 at 7:57 AM, Brooke Watson <watson@ecohealthalliance.org> wrote:
Hi team,

After our call yesterday, I wanted to share the following datasets with you all.

"GVP_spp_with_common_names" is an updated data table with the lists of species in each phase - I've added additional columns for Red List status and common name.

"Pteropus_virome_estimates" are the estimated number of viruses we would find with a given number of samples, based on Anthony et al. 2013. We used Simon's original data and the [iNEXT](#) Chao estimator in R to interpolate and extrapolate these values.

For Pteropus, we estimate that 51% of one species's virome can be found with 375 samples, 60% would take 560 samples, 70% requires 854, and 75% requires 1051. Confidence intervals around these estimates are in the chart.

"GVP_cost_chart" uses these estimates, along with the value from Anthony 2013 that states that 7079 samples would cost \$1.2 M, and does two things:

1. extrapolates these costs to all mammal species.
2. works backward based on a flat rate to find costs for 99, 95, 85 etc. % of the virome.
3. Adds these to the cost estimates for all waterfowl and "50 domestic species", which are included in the GVP *Science* paper.

Note that these are flat per-sample costs that don't differentiate between fixed and variable costs, so take that with a grain of salt. Also, as Peter mentioned, our Marxan-based target sampling only covers some 63% of the mammals in the world (an estimated 70% of the virome **if** these species are sampled to saturation), so if we're taking a percent of a percent, we should factor that into the way we discuss what we're providing.

Hopefully these are helpful in the next steps. Let me know if you have any questions.

Best,

Brooke

On Wed, Jun 28, 2017 at 6:45 PM, Brooke Watson <watson@ecohealthalliance.org> wrote:

Hi all,

Thanks for a productive call this afternoon. We discussed a lot of important parameters for the GVP and raised several questions.

Below are some questions that came up on the call that I think will help us refine the modeling and the pitch - I'd love the implementation team's input on the below:

1. Are there species that we should exclude a priori?
2. How many samples do we actually need per species? (2000? 1000?)
3. Should we group species into "high-sample" and "low-sample" species based on some factor (zoonotic risk, abundance/threat status, order?)
4. How do we rank the species?

5. What are the best estimates for rough fixed infrastructure costs?

Note - in the analyses presented during the May webinar, we have been using a fixed cost of \$1.5M per sample site.

Previous estimates have used PREDICT costs, roughly estimated at \$1 million/year/country.

6. Should infrastructure costs be calculated at the country level or the sampling unit level?
7. How much would 70% of the virome cost with these new parameters? 60%? 51%?
8. How long will each (the average) sampling unit cost to complete the GVP?

These will help refine the modeling. We're still at 10,000 feet, so rough estimates are fine, but (for example) it was good to learn that the fixed costs ought to be annualized, and if there are any other red flags that should be factored into the optimization site selection, please let me know.

I'll start working on questions 4 and 7 with Yasha, Kevin and Carlos. The items I most need input on are 5, 6, and 8.

Thanks everyone for your input!

Best,

Brooke

On Wed, Jun 28, 2017 at 5:20 PM, [REDACTED] wrote:

Hi Peter, Jonna and Brooke,

Cc David, Tracey and Chris

Please see the call-in information below for our meeting today:

GVP country budget call June 28 3pm PDT/6pm EST

[REDACTED] Access code [REDACTED]

Thank you for joining,

[REDACTED]

REDACTED

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EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

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